

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/833,245B
Source: /Fw/6
Date Processed by STIC: 9/12/05

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IFW16

RAW SEQUENCE LISTING DATE: 09/12/2005
 PATENT APPLICATION: US/09/833,245B TIME: 10:31:21

Input Set : N:\DA\pto.da.txt
 Output Set: N:\CRF4\09122005\I833245B.raw

4 <110> APPLICANT: Human Genome Sciences, Inc.
 6 <120> TITLE OF INVENTION: Albumin Fusion Proteins
 8 <130> FILE REFERENCE: PF546
 10 <140> CURRENT APPLICATION NUMBER: 09/833,245B
 11 <141> CURRENT FILING DATE: 2001-04-12
 13 <160> NUMBER OF SEQ ID NOS: 2279
 15 <170> SOFTWARE: PatentIn Ver. 2.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 23
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Artificial Sequence
 22 <220> FEATURE:
 23 <221> NAME/KEY: primer_bind
 24 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
 26 <400> SEQUENCE: 1
 27 cccaagaatt cccttatcca ggc 23
 30 <210> SEQ ID NO: 2
 31 <211> LENGTH: 33
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Artificial Sequence
 35 <220> FEATURE:
 36 <221> NAME/KEY: primer_bind
 37 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
 39 <400> SEQUENCE: 2
 40 gggaaagctta gaaggccacag gatccctcca cag 33
 43 <210> SEQ ID NO: 3
 44 <211> LENGTH: 16
 45 <212> TYPE: DNA
 46 <213> ORGANISM: Artificial Sequence
 48 <220> FEATURE:
 49 <221> NAME/KEY: misc_structure
 50 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
 51 with non-cohesive ends.
 53 <400> SEQUENCE: 3 16
 54 gataaaagatt cccaac
 57 <210> SEQ ID NO: 4
 58 <211> LENGTH: 17
 59 <212> TYPE: DNA
 60 <213> ORGANISM: Artificial Sequence
 62 <220> FEATURE:
 63 <221> NAME/KEY: misc_structure
 64 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
 65 with non-cohesive ends.

JMP 6-7

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67 <400> SEQUENCE: 4
 68 aattgttggg aatcttt 17
 71 <210> SEQ ID NO: 5
 72 <211> LENGTH: 17
 73 <212> TYPE: DNA
 74 <213> ORGANISM: Artificial Sequence
 76 <220> FEATURE:
 77 <221> NAME/KEY: misc_structure
 78 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
 79 with non-cohesive ends.
 81 <400> SEQUENCE: 5 17
 82 ttaggcttat tcccaac
 85 <210> SEQ ID NO: 6
 86 <211> LENGTH: 18
 87 <212> TYPE: DNA
 88 <213> ORGANISM: Artificial Sequence
 90 <220> FEATURE:
 91 <221> NAME/KEY: misc_structure
 92 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
 93 with non-cohesive ends.
 95 <400> SEQUENCE: 6
 96 aattgttggg aataagcc 18
 99 <210> SEQ ID NO: 7
 100 <211> LENGTH: 24
 101 <212> TYPE: PRT
 102 <213> ORGANISM: Artificial Sequence
 104 <220> FEATURE:
 105 <221> NAME/KEY: SITE
 106 <222> LOCATION: 1)..(19)
 107 <223> OTHER INFORMATION: invertase leader sequence
 109 <220> FEATURE:
 110 <221> NAME/KEY: SITE
 111 <222> LOCATION: 20)..(24)
 112 <223> OTHER INFORMATION: first 5 amino acids of mature human serum albumin
 114 <400> SEQUENCE: 7
 115 Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys
 116 1 5 10 15
 118 Ile Ser Ala Asp Ala His Lys Ser
 119 20
 122 <210> SEQ ID NO: 8
 123 <211> LENGTH: 21
 124 <212> TYPE: DNA
 125 <213> ORGANISM: Artificial Sequence
 127 <220> FEATURE:
 128 <221> NAME/KEY: misc_structure
 129 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
 130 fragments with non-cohesive ends.
 132 <400> SEQUENCE: 8
 133 gagatgcaca cctgagtgag g 21

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136 <210> SEQ ID NO: 9
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138 <212> TYPE: DNA
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141 <220> FEATURE:
142 <221> NAME/KEY: misc_structure
143 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
144     fragments with non-cohesive ends.
146 <400> SEQUENCE: 9
147 gatcctgtgg cttcgatgca cacaaga                                27
150 <210> SEQ ID NO: 10
151 <211> LENGTH: 24
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <221> NAME/KEY: misc_structure
157 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
158     fragments with non-cohesive ends.
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161 ctcttgtgtg catcgaagcc acag                                24
164 <210> SEQ ID NO: 11
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167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
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171 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
172     fragments with non-cohesive ends.
174 <400> SEQUENCE: 11
175 tgtgaaagag cctcagaatt tattcccaac                                30
178 <210> SEQ ID NO: 12
179 <211> LENGTH: 31
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <221> NAME/KEY: misc_structure
185 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
186     fragments with non-cohesive ends.
188 <400> SEQUENCE: 12
189 aattgttggg aataaattct gaggctttc c                                31
192 <210> SEQ ID NO: 13
193 <211> LENGTH: 47
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <221> NAME/KEY: misc_structure
199 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
200     fragments with non-cohesive ends.
202 <400> SEQUENCE: 13

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203 ttaggcttag gtggcggtgg atccggcggt ggtggatctt tcccaac 47
 206 <210> SEQ ID NO: 14
 207 <211> LENGTH: 48
 208 <212> TYPE: DNA
 209 <213> ORGANISM: Artificial Sequence
 211 <220> FEATURE:
 212 <221> NAME/KEY: misc_structure
 213 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
 214 fragments with non-cohesive ends.
 216 <400> SEQUENCE: 14
 217 aattgttggg aaagatccac caccgcccga tccaccgcga cctaagcc 48
 220 <210> SEQ ID NO: 15
 221 <211> LENGTH: 62
 222 <212> TYPE: DNA
 223 <213> ORGANISM: Artificial Sequence
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 226 <221> NAME/KEY: misc_structure
 227 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
 228 fragments with non-cohesive ends.
 230 <400> SEQUENCE: 15
 231 ttaggcttag gcgggtgggtgg atctggtggc ggccggatctg gtggcggtgg atccccc 60
 233 ac 62
 236 <210> SEQ ID NO: 16
 237 <211> LENGTH: 63
 238 <212> TYPE: DNA
 239 <213> ORGANISM: Artificial Sequence
 241 <220> FEATURE:
 242 <221> NAME/KEY: misc_structure
 243 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
 244 fragments with non-cohesive ends.
 246 <400> SEQUENCE: 16
 247 aattgttggg aaggatccac cgccaccaga tccgcccgcga ccagatccac caccgcctaa 60
 249 gcc 63
 252 <210> SEQ ID NO: 17
 253 <211> LENGTH: 1782
 254 <212> TYPE: DNA
 255 <213> ORGANISM: Homo sapiens
 257 <220> FEATURE:
 258 <221> NAME/KEY: CDS
 259 <222> LOCATION: (1)..(1755)
 262 <400> SEQUENCE: 17
 263 gat gca cac aag agt gag gtt gct cat cgg ttt aaa gat ttg gga gaa 48
 264 Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 265 1 5 10 15
 267 gaa aat ttc aaa gcc ttg gtg att gcc ttt gct cag tat ctt cag 96
 268 Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 269 20 25 30
 271 cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa 144
 272 Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

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273	35	40	45	
275	ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa			192
276	Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys			
277	50	55	60	
279	tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt			240
280	Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu			
281	65	70	75	80
283	cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct			288
284	Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro			
285	85	90	95	
287	gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc			336
288	Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu			
289	100	105	110	
291	ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat			384
292	Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His			
293	115	120	125	
295	gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga			432
296	Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg			
297	130	135	140	
299	aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg			480
300	Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg			
301	145	150	155	160
303	tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc			528
304	Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala			
305	165	170	175	
307	tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg			576
308	Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser			
309	180	185	190	
311	tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa			624
312	Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu			
313	195	200	205	
315	aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc			672
316	Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro			
317	210	215	220	
319	aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa			720
320	Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys			
321	225	230	235	240
323	gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac			768
324	Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp			
325	245	250	255	
327	agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc			816
328	Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser			
329	260	265	270	
331	agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac			864
332	Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His			
333	275	280	285	
335	tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca			912
336	Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser			
337	290	295	300	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:25; N Pos. 18,19,20,21,22,23,24,25,26,27,28,29,30,31,32
Seq#:26; N Pos. 37,38,39,40,41,42,43,44,45,46,47,48,49,50,51
Seq#:27; N Pos. 19,20,21,22,23,24,25,26,27,28,29,30,31,32,33
Seq#:28; N Pos. 38,39,40,41,42,43,44,45,46,47,48,49,50,51,52
Seq#:32; N Pos. 29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46
Seq#:33; N Pos. 38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55
Seq#:74; Xaa Pos. 24
Seq#:76; Xaa Pos. 5
Seq#:77; Xaa Pos. 29,34,37
Seq#:78; Xaa Pos. 3,17,33
Seq#:82; Xaa Pos. 196,224,233
Seq#:83; Xaa Pos. 60,73,75,82
Seq#:86; Xaa Pos. 26
Seq#:87; Xaa Pos. 50
Seq#:89; Xaa Pos. 41
Seq#:91; Xaa Pos. 13
Seq#:95; Xaa Pos. 12,38,43,145
Seq#:99; Xaa Pos. 260
Seq#:101; Xaa Pos. 259,262,280
Seq#:104; Xaa Pos. 42,49,69,76
Seq#:115; Xaa Pos. 12,49,51
Seq#:124; Xaa Pos. 7,22,24,111
Seq#:125; Xaa Pos. 81,84
Seq#:127; Xaa Pos. 1,19,81
Seq#:131; Xaa Pos. 142
Seq#:137; Xaa Pos. 42
Seq#:146; Xaa Pos. 131,185,218,220,250,312
Seq#:154; Xaa Pos. 91,93,99
Seq#:158; Xaa Pos. 36
Seq#:159; Xaa Pos. 10,19
Seq#:163; Xaa Pos. 2,6,14,34,51
Seq#:169; Xaa Pos. 6,13,51
Seq#:170; Xaa Pos. 33,129
Seq#:175; Xaa Pos. 44,57
Seq#:176; Xaa Pos. 26
Seq#:180; Xaa Pos. 71
Seq#:181; Xaa Pos. 1,5,8
Seq#:189; Xaa Pos. 21
Seq#:190; Xaa Pos. 15,30,32,187
Seq#:195; Xaa Pos. 3,17
Seq#:196; Xaa Pos. 26,28
Seq#:197; Xaa Pos. 2
Seq#:198; Xaa Pos. 27
Seq#:200; Xaa Pos. 8,12,16,18,19,23

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Seq#:204; Xaa Pos. 9,21
Seq#:211; Xaa Pos. 79,321
Seq#:215; Xaa Pos. 8,11,18,61
Seq#:216; Xaa Pos. 8,11,18,61
Seq#:223; Xaa Pos. 36,37
Seq#:228; Xaa Pos. 98
Seq#:234; Xaa Pos. 15

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2270; Line(s) 91695
Seq#:2271; Line(s) 91709
Seq#:2276; Line(s) 91778

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L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:880 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
L:970 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
L:1176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:1280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:1847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:16
L:1901 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:0
L:1945 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77 after pos.:16
M:341 Repeated in SeqNo=77
L:1980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:0
M:341 Repeated in SeqNo=78
L:2297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:192
M:341 Repeated in SeqNo=82
L:2349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:48
M:341 Repeated in SeqNo=83
L:2459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:16
L:2490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:48
L:2550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:89 after pos.:32
L:2589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91 after pos.:0
L:2686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95 after pos.:0
M:341 Repeated in SeqNo=95
L:2816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:99 after pos.:256
L:2985 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:256
M:341 Repeated in SeqNo=101
L:3191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:32
M:341 Repeated in SeqNo=104
L:3507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115 after pos.:0
M:341 Repeated in SeqNo=115
L:3695 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:124 after pos.:0
M:341 Repeated in SeqNo=124
L:3752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:125 after pos.:80
L:3894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:127 after pos.:0
M:341 Repeated in SeqNo=127
L:4006 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131 after pos.:128
L:4170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137 after pos.:32
L:4527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:146 after pos.:128
M:341 Repeated in SeqNo=146
L:4780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:154 after pos.:80
M:341 Repeated in SeqNo=154
L:4868 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:158 after pos.:32
L:4901 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:159 after pos.:0
M:341 Repeated in SeqNo=159
L:5102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:163 after pos.:0
M:341 Repeated in SeqNo=163
L:5240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:169 after pos.:0
M:341 Repeated in SeqNo=169
L:5279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:170 after pos.:32

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M:341 Repeated in SeqNo=170

L:5410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:175 after pos.:32